

EXHIBIT 3

DR EMBL; AE004969; AAW89056.1; -; Genomic_DNA.
DR RefSeq; YP_207468.1; -.
DR HSSP; P13000; 1BYI.
DR STRING; Q5F9T1; -.
DR GeneID; 3281703; -.
DR GenomeReviews; AE004969_GR; NGO0309.
DR KEGG; ngo:NGO0309; -.
DR NMPDR; fig|242231.4.peg.499; -.
DR HOGENOM; HBG650065; -.
DR OMA; LLTIDYI; -.
DR BioCyc; NGON242231:NGO0309-MON; -.
DR GO; GO:0005524; F:ATP binding; IEA:HAMAP.
DR GO; GO:0004141; F:dethiobiotin synthase activity; IEA:HAMAP.
DR GO; GO:0000287; F:magnesium ion binding; IEA:HAMAP.
DR GO; GO:0009102; P:biotin biosynthetic process; IEA:HAMAP.
DR HAMAP; MF_00336; -; 1.
DR InterPro; IPR004472; BioD_synth.
DR PIRSF; PIRSF006755; DTB_synth; 1.
PE 3: Inferred from homology;
KW ATP-binding; Biotin biosynthesis; Complete proteome; Ligase;
KW Magnesium; Nucleotide-binding.
FT CHAIN 1 215 Dethiobiotin synthetase.
FT /FTId=PRO_0000302532.
FT NP_BIND 9 17 ATP (By similarity).
SQ SEQUENCE 215 AA; 23676 MW; 48CB57B353B7CD95 CRC64;
MKGVYFVSGI DTDIGKTVAT GMLAKQLLQQ GKSVITQKPV QTGCQDIAED IAVHRKIMGI
PMQEAEDEQRL TMPEIFSHPA SPHLAARLDG RGLDLDKIRT ATQELAAQYE VVLVEGAGGL
MVPLTEKLLT IDHIQQQAYP VILVTSGR LG SINHTLLSFV VLKQYGIRLH SLVFNHIHDS
RDAHVAQDSL NYLQCRLKAD FPEAEWMELA KTGAV

DR EMBL; AE004969; AAW90296.1; ALT_INIT; Genomic_DNA.
DR RefSeq; YP_208708.1; -.
DR STRING; Q5F691; -.
DR GeneID; 3281272; -.
DR GenomeReviews; AE004969_GR; NGO1671.
DR KEGG; ngo:NGO1671; -.
DR NMPDR; fig|242231.4.peg.1812; -.
DR HOGENOM; HBG650290; -.
DR OMA; IIAREVV; -.
DR BioCyc; NGON242231:NGO1671-MON; -.
DR GO; GO:0005737; C:cytoplasm; IEA:UniProtKB-SubCell.
DR GO; GO:0005524; F:ATP binding; IEA:HAMAP.
DR GO; GO:0004140; F:dephospho-CoA kinase activity; IEA:HAMAP.
DR GO; GO:0015937; P:coenzyme A biosynthetic process; IEA:HAMAP.
DR HAMAP; MF_00376; -; 1.
DR InterPro; IPR001977; Depp_CoAkinase.
DR PROSITE; PS51219; DPKC; 1.
PE 3: Inferred from homology;
KW ATP-binding; Coenzyme A biosynthesis; Complete proteome;
Cytoplasm;
KW Kinase; Nucleotide-binding; Transferase.
FT CHAIN 1 210 Dephospho-CoA kinase.

FT /FTid=PRO_0000243307.
 FT DOMAIN 4 202 DPCK.
 FT NP_BIND 9 16 ATP (Potential).
 SQ SEQUENCE 210 AA; 22950 MW; 1443ED0A3D4057B5 CRC64;
 MTAWVGLTGG IGSGKSAAAQ YFADLGVPRI DADAAHSLT ASDGIALPEI RRLFGDTVFD
 TQGLLRDIL RKEIFASPSR KALLESVMLP LIFSEIKKQQ ETFTDAVYGI VEIPLLTEKR
 QFISLIRRVL TISAPLEKRI GRVMARSLT RGEVADIISH QASESERLLL ADDVLLNDGS
 LKSLREKTML LHAFYSGIFA SKPTQKGHNG
 //

DR EMBL; AE004969; AAW88861.1; ALT_INIT; Genomic_DNA.
 DR RefSeq; YP_207273.1; -.
 DR HSSP; P0A6P7; 1PUI.
 DR STRING; Q5FAC6; -.
 DR GeneID; 3282443; -.
 DR GenomeReviews; AE004969_GR; NGO0100.
 DR KEGG; ngo:NGO0100; -.
 DR NMPDR; fig|242231.4.peg.842; -.
 DR HOGENOM; HBG447097; -.
 DR OMA; THFVTS; -.
 DR BioCyc; NGON242231:NGO0100-MON; -.
 DR GO; GO:0005622; C:intracellular; IEA:InterPro.
 DR GO; GO:0005525; F:GTP binding; IEA:HAMAP.
 DR GO; GO:0000917; P:barrier septum formation; IEA:HAMAP.
 DR GO; GO:0007049; P:cell cycle; IEA:UniProtKB-KW.
 DR HAMAP; MF_00321; -; 1.
 DR InterPro; IPR019987; GTP-bd_ribosome_bio_YsxC.
 DR InterPro; IPR002917; MMR_HSR1_GTP_bd.
 DR Pfam; PF01926; MMR_HSR1; 1.
 PE 3: Inferred from homology;
 KW Cell cycle; Cell division; Complete proteome; GTP-binding;
 KW Nucleotide-binding; Septation.
 FT CHAIN 1 209 Probable GTP-binding protein engB.
 FT /FTid=PRO_0000266903.
 FT NP_BIND 30 37 GTP (Potential).
 FT NP_BIND 75 79 GTP (Potential).
 FT NP_BIND 142 145 GTP (Potential).
 SQ SEQUENCE 209 AA; 23600 MW; 79742D484A0A1ABF CRC64;
 MNLFQNAKFF TTVNHLKDLP DTPLEIAFVG RSNAGKSSAI NTLTNHVRLA YVSKTPGRTQ
 HINFFELQNG NFMVDLPYG YAQVPEAVRA HWVNLLGDYL RHRKQLIGLV LIMDARHPLK
 ELDIRMLDFF HTTGRPVHIL LSKADKLSKN EQIKTLSQVK KLLKPYSRQ NISVQLFSSL
 KKQGIDEANR TVGSWFDAAD AAASSPEEN
 //

DR EMBL; AE004969; AAW89897.1; -; Genomic_DNA.

DR RefSeq; YP_208309.1; -.
 DR STRING; Q5F7E0; -.
 DR GeneID; 3282595; -.
 DR GenomeReviews; AE004969_GR; NGO1238.
 DR KEGG; ngo:NGO1238; -.
 DR NMPDR; fig|242231.4.peg.1300; -.
 DR HOGENOM; HBG391868; -.
 DR OMA; LLMFRAE; -.
 DR BioCyc; NGON242231:NGO1238-MON; -.
 DR GO; GO:0005737; C:cytoplasm; IEA:UniProtKB-SubCell.
 DR GO; GO:0005524; F:ATP binding; IEA:UniProtKB-KW.
 DR GO; GO:0003879; F:ATP phosphoribosyltransferase activity;
 IEA:HAMAP.
 DR GO; GO:0000105; P:histidine biosynthetic process; IEA:HAMAP.
 DR HAMAP; MF_01018; -; 1.
 DR InterPro; IPR001348; ATP_PRibTrfase.
 DR InterPro; IPR013820; ATP_PRibTrfase_cat.
 DR InterPro; IPR018198; ATP_PRibTrfase_CS.
 DR PANTHER; PTHR21403; ATP_phospho_trans; 1.
 DR Pfam; PF01634; HisG; 1.
 DR PROSITE; PS01316; ATP_P_PHORIBOSYLTR; 1.
 PE 3: Inferred from homology;
 KW Amino-acid biosynthesis; ATP-binding; Complete proteome;
 Cytoplasm;
 KW Glycosyltransferase; Histidine biosynthesis; Nucleotide-binding;
 KW Transferase.
 FT CHAIN 1 221 ATP phosphoribosyltransferase.
 FT /FTId=PRO_0000229320.
 SQ SEQUENCE 221 AA; 23776 MW; 74D2248667173BD0 CRC64;
 MQDNALTIAL SKGRIFEETL PLLAAAGIAP TEEPEKSRKL IIGTNHENIR LVIVRATDVP
 TYVRYGAADF GIAGKDVLIIE HGGTGLYRPL DLEIAKCRMM VAVRKGFDYE AASQPGCRLK
 IATKYPEIAA SHFAGKGVHV DIIKLYGSME LAPLVGLSDA IVDLVSTGNT LKANGLEAVE
 HIVDISSYLV VNKAALKTKY ALLEPIIQSF GGAVKAKWAF I

DR EMBL; AE004969; AAW88966.1; -; Genomic_DNA.
 DR RefSeq; YP_207378.1; -.
 DR STRING; Q5FA21; -.
 DR GeneID; 3281167; -.
 DR GenomeReviews; AE004969_GR; NGO0213.
 DR KEGG; ngo:NGO0213; -.
 DR NMPDR; fig|242231.4.peg.252; -.
 DR HOGENOM; HBG292341; -.
 DR OMA; SVRFAFE; -.
 DR BioCyc; NGON242231:NGO0213-MON; -.
 DR GO; GO:0005737; C:cytoplasm; IEA:UniProtKB-SubCell.
 DR GO; GO:0000107; F:imidazoleglycerol-phosphate synthase activity;
 IEA:HAMAP.
 DR GO; GO:0006541; P:glutamine metabolic process; IEA:UniProtKB-KW.
 DR GO; GO:0000105; P:histidine biosynthetic process; IEA:HAMAP.
 DR HAMAP; MF_00278; -; 1.
 DR InterPro; IPR017926; GATASE_1.
 DR InterPro; IPR000991; GATase_class1_C.
 DR InterPro; IPR010139; Imidazole-glycPsynth_HisH.
 DR InterPro; IPR016226; Imidazole-GPS_HisH.
 DR Pfam; PF00117; GATase; 1.

DR PIRSF; PIRSF000495; Amidotransf_hisH; 1.
 DR PROSITE; PS51273; GATASE_TYPE_1; 1.
 PE 3: Inferred from homology;
 KW Amino-acid biosynthesis; Complete proteome; Cytoplasm;
 KW Glutamine amidotransferase; Histidine biosynthesis; Transferase.
 FT CHAIN 1 212 Imidazole glycerol phosphate synthase
 FT subunit hisH.
 FT /FTId=PRO_0000231736.
 FT DOMAIN 2 212 Glutamine amidotransferase type-1.
 FT ACT_SITE 85 85 Nucleophile (By similarity).
 FT ACT_SITE 194 194 By similarity.
 FT ACT_SITE 196 196 By similarity.
 SQ SEQUENCE 212 AA; 23570 MW; BDDFE90E1A43ED5A CRC64;
 MQTAIIDYGM GNLHSVLSKV RTAGQLAGKN TKIFLSGDPD RVSRADKVIF PGQGAMPDCM
 AALTRGGLDE AVKDALKNKP FFGICVGAQL LFDHSEEGNT DGLGWFGGKV RRFARDLRDP
 QGCRLKVPFH GWNTVRQTQN HPLFQGIPQN TRFYFVHSYY FAPENPETIL GESDYPSPFA
 CIVGKDNVFA TQFHTEKSHD AGLTMLKNFL NW

DR EMBL; AE004969; AAW90546.1; -; Genomic_DNA.
 DR RefSeq; YP_208958.1; -.
 DR STRING; Q5F5J1; -.
 DR GeneID; 3282686; -.
 DR GenomeReviews; AE004969_GR; NGO1933.
 DR KEGG; ngo:NGO1933; -.
 DR NMPDR; fig|242231.4.peg.1749; -.
 DR HOGENOM; Q5F5J1; -.
 DR OMA; GACYHDL; -.
 DR PhylomeDB; Q5F5J1; -.
 DR BioCyc; NGON242231:NGO1933-MON; -.
 DR GO; GO:0008936; F:nicotinamidase activity; IEA:EC.
 DR GO; GO:0008152; P:metabolic process; IEA:InterPro.
 DR InterPro; IPR000868; Isochorismatase-like.
 DR Gene3D; G3DSA:3.40.50.850; Isochorismatase_hydro; 1.
 DR Pfam; PF00857; Isochorismatase; 1.
 PE 4: Predicted;
 KW Complete proteome; Hydrolase.
 SQ SEQUENCE 211 AA; 23439 MW; D1EFDE053D35A3EC CRC64;
 MIVSIDVDAQ KTFTPLCPDE LPVNEGHLIV EELNAQAALA DLRVMTKDAH HMAAKWLVDN
 PVDMLKPTGF SDADLTWVAH AMVGTRGYEL LDGLPSVKEY DYCVMKGVDV ELHPYGACFH
 DIEEKLSTGL IEWLRQNTN MVIVGGLATD YCVKTTVLQL LKGGRWQVIV NEAACRGIAP
 DTIEAAWQEM RSSGAILKN AEKIKKYINN Q

DR EMBL; AE004969; AAW90184.1; -; Genomic_DNA.
 DR RefSeq; YP_208596.1; -.
 DR STRING; Q5F6K3; -.
 DR GeneID; 3281487; -.
 DR GenomeReviews; AE004969_GR; NGO1548.
 DR KEGG; ngo:NGO1548; -.
 DR NMPDR; fig|242231.4.peg.1610; -.
 DR HOGENOM; Q5F6K3; -.
 DR OMA; YERIAQP; -.
 DR PhylomeDB; Q5F6K3; -.
 DR BioCyc; NGON242231:NGO1548-MON; -.

DR GO; GO:0030288; C:outer membrane-bounded periplasmic space;
IEA:InterPro.
DR GO; GO:0003756; F:protein disulfide isomerase activity; IEA:EC.
DR GO; GO:0015035; F:protein disulfide oxidoreductase activity;
IEA:InterPro.
DR GO; GO:0045454; P:cell redox homeostasis; IEA:InterPro.
DR InterPro; IPR001853; OxRdtase_DSBA.
DR InterPro; IPR017936; Thioredoxin-like.
DR InterPro; IPR012336; Thioredoxin-like_fold.
DR InterPro; IPR017937; Thioredoxin_CS.
DR InterPro; IPR012335; Thioredoxin_fold.
DR Gene3D; G3DSA:3.40.30.10; Thioredoxin_fold; 1.
DR Pfam; PF01323; DSBA; 1.
DR PROSITE; PS00194; THIOREDOXIN_1; 1.
DR PROSITE; PS51352; THIOREDOXIN_2; 1.
PE 4: Predicted;
KW Complete proteome; Isomerase.
SQ SEQUENCE 214 AA; 24003 MW; 31A85BBA5EB3CE18 CRC64;
MKFKHLLPLL LSAVLSAQAY ALTEGEDYLV LDKPIPQEQP GKIEVLEFFG YFCVHCHHFD
PLLLKLGLKAL PSDTYLRTEH VVWRPEMLGL ARMAAAVKLS GLKYQANSV FKAVYEQKIR
LENRAVAGKW ALSQKGF DGK KLMRAYDSPE AAVALKMQK LTEQYGIDST PTVIVGGKYR
VIFNNGFDGG VHTIKELVAK VREERKRQTP AVQK

DR EMBL; AE004969; AAW90118.1; -; Genomic_DNA.
DR RefSeq; YP_208530.1; -.
DR STRING; Q5F6R9; -.
DR GeneID; 3281613; -.
DR GenomeReviews; AE004969_GR; NGO1479.
DR KEGG; ngo:NGO1479; -.
DR NMPDR; fig|242231.4.peg.1454; -.
DR HOGENOM; Q5F6R9; -.
DR PhylomeDB; Q5F6R9; -.
DR BioCyc; NGON242231:NGO1479-MON; -.
PE 4: Predicted;
KW Complete proteome.
SQ SEQUENCE 209 AA; 23458 MW; B72DD3AA633EB0D3 CRC64;
MEVQLPKIKT VRVMLAGMTA QQESVFKMAF KMHNTTRYET VSPSDGSAV DLVLADTDAE
GGFELWKELA GRYKAIPVAV CSEKVPDSEV PYLPKPIRFE TLFPMRLKLL QGENVYGKSF
IAPADRSASN NGNVQRTVTI RQFNPNKGLL GALRFAEKNR QDIAILHGK PVLNCFPLDT
TGFADRKCVK TRRIVQRRKF AGQLQDCSR

DR EMBL; AE004969; AAW90087.1; -; Genomic_DNA.
DR RefSeq; YP_208499.1; -.
DR STRING; Q5F6V0; -.
DR GeneID; 3281693; -.
DR GenomeReviews; AE004969_GR; NGO1445.
DR KEGG; ngo:NGO1445; -.
DR NMPDR; fig|242231.4.peg.1423; -.
DR HOGENOM; Q5F6V0; -.
DR OMA; ETRANAY; -.
DR PhylomeDB; Q5F6V0; -.
DR BioCyc; NGON242231:NGO1445-MON; -.
DR GO; GO:0019867; C:outer membrane; IEA:InterPro.
DR GO; GO:0009405; P:pathogenesis; IEA:InterPro.
DR InterPro; IPR008640; Hep_Hag.

DR Pfam; PF05658; Hep_Hag; 4.
 PE 4: Predicted;
 KW Complete proteome.
 SQ SEQUENCE 222 AA; 22826 MW; C024A19C5373E774 CRC64;
 MGLRQKLRGI IPNLATSIGT SAEANAPGAL ALGGSSEASK KFSIAEGYLA SSDGYGAIAI
 GSAAKIKQLE KGTINHIVGN DNKGLYVDAD GNVTKITVRT ESEKDILSRY GQTYGAVALG
 FRSSSHNLFA SSFGAFSTAT AIESLAVGDS SQSTGYRSAT FGSHSRALAE ESLALGYETR
 ANAYGSVALG AESVANEENT VSVSSDTLKR KIVNVADGTE DL

DR EMBL; AE004969; AAW90078.1; -; Genomic_DNA.
 DR RefSeq; YP_208490.1; -.
 DR GeneID; 3281702; -.
 DR GenomeReviews; AE004969_GR; NGO1435.
 DR KEGG; ngo:NGO1435; -.
 DR NMPDR; fig|242231.4.peg.767; -.
 DR HOGENOM; Q5F6V9; -.
 DR OMA; FFARANT; -.
 DR PhylomeDB; Q5F6V9; -.
 DR BioCyc; NGON242231:NGO1435-MON; -.
 DR InterPro; IPR004676; Cd-R_transporter.
 DR InterPro; IPR018388; Cd-R_transporter_subgr.
 DR Pfam; PF03596; Cad; 1.
 DR TIGRFAMs; TIGR00779; cad; 1.
 PE 4: Predicted;
 KW Complete proteome.
 SQ SEQUENCE 208 AA; 23177 MW; 1297237EA5DD043C CRC64;
 MRCFMFSTVI TAAVLYIATA VDLLVILLIF FARANTRKEY RDIYIGQYLG SVILILVSLF
 LAFVLNYVPE KQVLGGLGLI PIYLGKVAI YDDCEGEKRA KKELDEKGLS KLVGIVALVT
 VASCGADNIG LFVPYFVTLD LVDLLVTLLV FLILIFVLVY TAQRLANISG VGEIVEKFSR
 WIMAVIYIGL GLFIIENNT IRTIISII